

H  
Park



1600

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/677,584**

**DATE: 03/11/2003**  
**TIME: 10:54:53**

**Input Set : A:\PTO.VSK.txt**  
**Output Set: N:\CRF4\03112003\I677584.raw**

2 <110> APPLICANT: DIVERSA CORPORATION  
 3 SHORT, Jay  
 W--> 4 <120> TITLE OF INVENTION: WHOLE CELL ENGINEERING BY MUTAGENIZING A SUBSTANTIAL PORTION  
 OF A  
 W--> 5 STARTING GENOME, COMBINING MUTATIONS, AND OPTIONALLY REPEATING  
 7 <130> FILE REFERENCE: DIVER1510WO-1  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/677,584  
 C--> 10 <141> CURRENT FILING DATE: 2000-09-30  
 12 <150> PRIOR APPLICATION NUMBER: US 09/677,584  
 13 <151> PRIOR FILING DATE: 2000-09-30  
 15 <150> PRIOR APPLICATION NUMBER: US 09/594,459  
 16 <151> PRIOR FILING DATE: 2000-06-14  
 18 <160> NUMBER OF SEQ ID NOS: 33  
 20 <170> SOFTWARE: PatentIn version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 5818  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Escherichia coli  
 27 <400> SEQUENCE: 1  
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 30 ttccatgtga cctcttaca tggtaacgtt catgataact tctgtcttc atcgtgcggc 120  
 32 cgactggct aaatctgtgt tctcttcggc ggcgtgggt gatcgtcgcc gtactgccc 180  
 34 cttggtaac gtcgcgcgc aattggcaaa atattctggt aaatcaataa ccatctcatc 240  
 36 agagggtagt gaagccatgc agaaggcgc ttaccgatt taccgcaatc ccaacgtttc 300  
 38 tgccgaggcg atcagaaaagg ctggcgccat gcaaacagtc aagttggctc aggagttcc 360  
 40 cgaactgctg gccattgagg acaccaccc tttgagttat cgccaccagg tcgccaaga 420  
 42 gcttggcaag ctgggccta ttccaggataa atcccgccgaa tgggtgggttc actccgttct 480  
 44 cttgctcgag gccaccacat tccgcaccgt aggattactg catcaggagt ggtggatgcg 540  
 46 cccggatgac cctgccatg cgatgaaaaa ggagagtggc aatggctgg cagccgcgc 600  
 48 aactagccgg ttacgcattgg gcagcatgat gagcaacgtt attgcggctt gtgaccgcga 660  
 50 agccgatatt catgcttatac tgcaggacag gctggcgcat aacgagcgt tcgtggtgcg 720  
 52 ctccaagcac ccacgcaagg acgttagatc tgggtgtat ctgatcgacc atctgaagaa 780  
 54 ccaaccggag ttgggtggct atcagatca gattccgcaa aagggcgtgg tggataaacg 840  
 56 cggttaacgt aaaaatcgac cagccgc当地 ggcgagctt ggcgtcgca gtggcgcat 900  
 58 cacgctaaaa caggggata tcaacgtcaa cgcggtgctg gccgaggaga ttaaccgc当地 960  
 60 caagggtgag accccgttga aatggttgtt gctgaccggc gaaccggctg agtcgttagc 1020  
 62 ccaaggccttgc cgcgtcatcg acatttatac ccatcgctgg cggatcgagg agttccataa 1080  
 64 ggcattggaaa accggaggcag gagccgagag gcaacgcgt gaggaggccgg ataatctgga 1140  
 66 gcggatggtc tcgatcctt cgttgggtgc ggtcaggctg ttacagctca gagaaagctt 1200  
 68 cacgctgccc caagcactca gggcgcaagg gctgctaaag gaagcggaaac acgtagaaag 1260  
 70 ccagtccgca gaaacgggtgc tgacccggaa tgaatgtcag ctactggct atctggacaa 1320  
 72 gggaaaacgc aagcgcaaaag agaaaggcagg tagctgtcag tgggttaca tggcgatagc 1380  
 74 tagactggc ggttttatgg acagcaagcg aaccgaaatt gccagctgg ggcgcctctg 1440  
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82	gggcacaacaacaatcgctgtatccggctgtt	ccggctgtca	gcccaggggc	1680
84	gccccgttcttttgtcaagaccgacctgt	ccggtgccct	aatgaactcgaggacgagg	1740
86	cagcgcggctatcggtggctg	gccacgcgg	gcgttccctgcgcagctgt	1800
88	tcaactgaagcggaaaggggac	tggctgtctat	tggcgaagtggcggcag	1860
90	catctcaccttgctcctggc	gagaaagtatccatcat	ccatcatggctatgc	1920
92	atacgcttgcattccggcttacc	tgcccatcg	accaccaagc	1980
94	cacgtactcgatggaaagcc	ggtcttgcgt	atcaggatgatctggacgaa	2040
96	ggctcgcgcctggcgaacttgc	ttcgccaggc	tcaaggcgcgc	2100
98	tcgtcgacccatggcgat	gcctgttgc	cgaatatcat	2160
100	ctggattcatcgactgtggc	cggtgggttgc	tggcggaccgc	2220
102	ctacccgtatattgtgaa	gagcttggcg	gcgaatgggc	2280
104	acggtatcgccgtccat	tcgcagcgca	tcgccttcta	2340
106	tctgagcgggactctgggt	tcgaaatgac	cgaccaagc	2400
108	agatttcgatccaccggcc	ccttctatga	aagggtggc	2460
110	cgcggctggatgatctcc	agcgcgggg	tctcatgtgc	2520
112	gctcgatcccctcgcgagtt	gtttagctgc	ctgcctgagg	2580
114	ctaccggcagtgcaaatccg	tcggcatcca	gaaaccacgc	2640
116	tgcccccggaaatgcaggat	ggggaggc	gatggccgt	2700
118	gctcctgcgcctgatatacaga	acgaattgt	tgcaggatc	2760
120	tttccgccttggatactgc	gtggatggag	cgctggcgcc	2820
122	ctcaccacccactcgagctg	gataacttccc	gtccgcagg	2880
124	aaggtcgcgcgcattccgaa	tgaagaggcc	ggttaccgc	2940
126	caggcgccgcccggatgtt	ccgcctcgcc	gccccgc	3000
128	ggggccggggaccttgcaca	gatagcgtgg	tccggccagg	3060
130	ctctgcgacaatcgccgtcg	tctgcacgcg	ccgcgtcc	3120
132	ccgctacaggaaatgttcca	gccgttttc	cggttggcc	3180
134	cccgccgcacgcgtacgc	ccaacttgc	gccccgc	3240
136	ggcgacctgcaccacggaa	cgtgctcgac	ttcgccgacc	3300
138	ccgcacggatctcgccgaa	gctgttgc	gactatgc	3360
140	ctcagcgaccatcgccgatc	gttgcgatc	ctgcggggca	3420
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144	acgggcttgcgatcgccgt	gttcatcg	gacggcgac	3540
146	attgatctggatcgtaaacgc	catggc	cggttgc	3600
148	cacctgttcgtcgatgttgc	tcaggccgt	tcggcgt	3660
150	gccacacccgcgcctcgaa	gccctgcacc	aggccgc	3720
152	gactatggaaatgtgcggac	gatctggcc	agcaggcc	3780
154	ttggtggcgtatcgatgttgc	gacggtggag	ctgaaatgc	3840
156	tcgggtccacatcgatgttgc	cagcgttgc	tcgacgg	3900
158	gttttagcagtggccaaatggc	tgaggca	taggcatac	3960
160	gactggccgatcgccgt	cgccgcgg	cagcgt	4020
162	gtcgaaatcgatcgccgt	ttggcgcaggc	cgcaaggac	4080
164	cccgccggccatcgccgt	acggccagcg	cggttgcggc	4140
166	ggcgaaatggatgttgc	tgacgcca	gggttccagcc	4200
168	gaacagcgccatcgccgt	ttggggagca	gtcgccgc	4260
170	attggacgacatcgatgttgc	ggccctgtc	tcttgcata	4320
172	cagatccttgcgcgaa	agccatccag	tttactttgc	4380
174	gagggcgccccatcgatgttgc	ttccggcc	ataaaaccgc	4440

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176 tatcgccatg taagcccact gcaagctacc tgctttctct ttgcgcttgc gttttccctt	4500
178 gtccagatag cccagtagct gacattcatc cggggtcagc accgtttctg cgactggct	4560
180 ttctacgtgt tccgcttctt ttagcagccc ttgcgccttg agtgcgttgc gcagcgtgaa	4620
182 gctttctctg agctgtaaaca gcctgaccgc aacaaacgag aggatcgaga ccattccgctc	4680
184 cagattatcc ggctcctcca tgcgttgcct ctgcgttgcct gctccggttt tccatgcctt	4740
186 atggaactcc tcgatccgccc agcgatgggt ataaatgtcg atgacgcgca aggcttgggc	4800
188 tagcgactcg accggttcgc cggtcagcaa caaccatttc aacggggctt cacccttggg	4860
190 cgggttaatc tcctcgccca gcaccgcgtt gagcgtgata ttcccgtt ttagcgtgat	4920
192 gcccactg cgcaggctca agctcgcctt gcgggctggt cgattttac gtttaccgcg	4980
194 ttatccacc acgccctttt gcggaatgtct gatgtatag ccacccaact ccggttgggtt	5040
196 cttcagatgg tcgatcgat acaacccaga ctctacgtcc ttgcgttgggt gcttggagcg	5100
198 caccacgaag cgctcggtt ggcgcgcgtt gtcctgcaga taagcatgaa tattcggttc	5160
200 gcggtcacag accgcaatca cgttgctcat catgtgcctt atgcgttaacc ggctagttgc	5220
202 ggccgctgcc agccatttgc cacttcctt ttcatccgca tcggcagggtt catccggcg	5280
204 catccaccaac tcctgtatgca gtaatcctac ggtgcggaaat gtgggtggctt cgagcaagag	5340
206 aacggagtga acccaccatc cgcgggattt atcctgaata gagcccagct tgccaagctc	5400
208 ttcggcgcacc tggtggcgtt aactcaaaga ggtgggtgtcc tcaatggcca gcagttcggg	5460
210 aaactcctga gccaacctga ctgtttgcattt ggcgcgcagcc tttctgtatcg cctccggcaga	5520
212 aacgttggga ttgcgttaaaa atcgttaagc gccttcctgc atggcttcac taccctctga	5580
214 tgagatgggtt attgatttac cagaatattt tgccaaattgg gcggcgcacgt taaccaagcgt	5640
216 ggcagtacgg cgaggatcac ccagcgcgcgc cgaagagaac acagatttag cccagtcggc	5700
218 cgcacgatga agagcagaag ttatcatgaa cgttaccatg ttaggaggtc acatggaagt	5760
220 cagatcctgg aaaacgggaa aggttccgtt caggacgcta ctttgttata agagtcag	5818

223 <210> SEQ ID NO: 2

224 <211> LENGTH: 476

225 <212> TYPE: PRT

226 <213> ORGANISM: Escherichia coli

228 <400> SEQUENCE: 2

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231 1 5 10 15	
233 Phe Ser Ser Ala Ala Leu Gly Asp Pro Arg Arg Thr Ala Arg Leu Val	
234 20 25 30	
236 Asn Val Ala Ala Gln Leu Ala Lys Tyr Ser Gly Lys Ser Ile Thr Ile	
237 35 40 45	
239 Ser Ser Glu Gly Ser Glu Ala Met Gln Glu Gly Ala Tyr Arg Phe Tyr	
240 50 55 60	
242 Arg Asn Pro Asn Val Ser Ala Glu Ala Ile Arg Lys Ala Gly Ala Met	
243 65 70 75 80	
245 Gln Thr Val Lys Leu Ala Gln Glu Phe Pro Glu Leu Leu Ala Ile Glu	
246 85 90 95	
248 Asp Thr Thr Ser Leu Ser Tyr Arg His Gln Val Ala Glu Glu Leu Gly	
249 100 105 110	
251 Lys Leu Gly Ser Ile Gln Asp Lys Ser Arg Gly Trp Trp Val His Ser	
252 115 120 125	
254 Val Leu Leu Leu Glu Ala Thr Thr Phe Arg Thr Val Gly Leu Leu His	
255 130 135 140	
257 Gln Glu Trp Trp Met Arg Pro Asp Asp Pro Ala Asp Ala Asp Glu Lys	
258 145 150 155 160	
260 Glu Ser Gly Lys Trp Leu Ala Ala Ala Thr Ser Arg Leu Arg Met	

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**Output Set: N:\CRF4\03112003\I677584.raw**

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261           165           170           175
263 Gly Ser Met Met Ser Asn Val Ile Ala Val Cys Asp Arg Glu Ala Asp
264           180           185           190
266 Ile His Ala Tyr Leu Gln Asp Arg Leu Ala His Asn Glu Arg Phe Val
267           195           200           205
269 Val Arg Ser Lys His Pro Arg Lys Asp Val Glu Ser Gly Leu Tyr Leu
270           210           215           220
272 Ile Asp His Leu Lys Asn Gln Pro Glu Leu Gly Gly Tyr Gln Ile Ser
273 225           230           235           240
275 Ile Pro Gln Lys Gly Val Val Asp Lys Arg Gly Lys Arg Lys Asn Arg
276           245           250           255
278 Pro Ala Arg Lys Ala Ser Leu Ser Leu Arg Ser Gly Arg Ile Thr Leu
279           260           265           270
281 Lys Gln Gly Asn Ile Thr Leu Asn Ala Val Leu Ala Glu Glu Ile Asn
282           275           280           285
284 Pro Pro Lys Gly Glu Thr Pro Leu Lys Trp Leu Leu Leu Thr Gly Glu
285           290           295           300
287 Pro Val Glu Ser Leu Ala Gln Ala Leu Arg Val Ile Asp Ile Tyr Thr
288 305           310           315           320
290 His Arg Trp Arg Ile Glu Glu Phe His Lys Ala Trp Lys Thr Gly Ala
291           325           330           335
293 Gly Ala Glu Arg Gln Arg Met Glu Glu Pro Asp Asn Leu Glu Arg Met
294           340           345           350
296 Val Ser Ile Leu Ser Phe Val Ala Val Arg Leu Leu Gln Leu Arg Glu
297           355           360           365
299 Ser Phe Thr Leu Pro Gln Ala Leu Arg Ala Gln Gly Leu Leu Lys Glu
300           370           375           380
302 Ala Glu His Val Glu Ser Gln Ser Ala Glu Thr Val Leu Thr Pro Asp
303 385           390           395           400
305 Glu Cys Gln Leu Leu Gly Tyr Leu Asp Lys Gly Lys Arg Lys Arg Lys
306           405           410           415
308 Glu Lys Ala Gly Ser Leu Gln Trp Ala Tyr Met Ala Ile Ala Arg Leu
309           420           425           430
311 Gly Gly Phe Met Asp Ser Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala
312           435           440           445
314 Leu Trp Glu Gly Trp Glu Ala Leu Gln Ser Lys Leu Asp Gly Phe Leu
315           450           455           460
317 Ala Ala Lys Asp Leu Met Ala Gln Gly Ile Lys Ile
318 465           470           475
320 <210> SEQ ID NO: 3
321 <211> LENGTH: 30
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Defined sequence kernel
328 <220> FEATURE:
329 <221> NAME/KEY: misc_feature
330 <222> LOCATION: (1)..(30)
331 <223> OTHER INFORMATION: n is A, T, G, or C

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333 <400> SEQUENCE: 3	
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337 <210> SEQ ID NO: 4	
338 <211> LENGTH: 30	
339 <212> TYPE: DNA	
340 <213> ORGANISM: Artificial sequence	
342 <220> FEATURE:	
343 <223> OTHER INFORMATION: Defined sequence kernel	
345 <220> FEATURE:	
346 <221> NAME/KEY: misc_feature	
347 <222> LOCATION: (1)..(30)	
348 <223> OTHER INFORMATION: n is A, T, G, or C	
350 <400> SEQUENCE: 4	
<b>W--&gt; 351 nmnmnmnmnm nmnmnmnmnm mnmnmnmnm</b>	<b>30</b>
354 <210> SEQ ID NO: 5	
355 <211> LENGTH: 5	
356 <212> TYPE: PRT	
357 <213> ORGANISM: Artificial sequence	
359 <220> FEATURE:	
360 <223> OTHER INFORMATION: Antibody spacer peptide. The entire peptide sequence can be repeated more than one time	
363 <400> SEQUENCE: 5	
365 Gly Gly Gly Ser	
366 1 5	
368 <210> SEQ ID NO: 6	
369 <211> LENGTH: 14	
370 <212> TYPE: DNA	
371 <213> ORGANISM: Artificial sequence	
373 <220> FEATURE:	
374 <223> OTHER INFORMATION: Tetradecanucleotide d	
376 <400> SEQUENCE: 6	
377 catgccatgg catg	14
380 <210> SEQ ID NO: 7	
381 <211> LENGTH: 21	
382 <212> TYPE: DNA	
383 <213> ORGANISM: Artificial sequence	
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386 <223> OTHER INFORMATION: 21-mer d	
388 <400> SEQUENCE: 7	
389 aaatttgtca catcctgcag c	21
392 <210> SEQ ID NO: 8	
393 <211> LENGTH: 12	
394 <212> TYPE: DNA	
395 <213> ORGANISM: Artificial sequence	
397 <220> FEATURE:	
398 <223> OTHER INFORMATION: 12-mer target DNA	
400 <400> SEQUENCE: 8	
401 agccttagctg aa	12
404 <210> SEQ ID NO: 9	

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:12; Xaa Pos. 2  
Seq#:13; N Pos. 6,7,8,9,10  
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Seq#:17; N Pos. 116,117,118,119,120,121

**VERIFICATION SUMMARY**  
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Input Set : A:\PTO.VSK.txt  
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L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
M:341 Repeated in SeqNo=14  
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
M:341 Repeated in SeqNo=15  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
M:341 Repeated in SeqNo=16  
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
M:341 Repeated in SeqNo=17